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2. OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/016,496

DATE: 05/16/2002

TIME: 14:07:55

Input Set : N:\Crf3\RULE60\10016496.raw

Output Set: N:\CRF3\05162002\J016496.raw

ENTERED

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1 <110> APPLICANT: H. William Harris
2      Edward M. Brown
3      Steven C. Hebert
4 <120> TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
5      Species and Methods of Use Thereof
6 <130> FILE REFERENCE: 2856.1001-007
7 <140> CURRENT APPLICATION NUMBER: 10/016,496
8 <141> CURRENT FILING DATE: 2001-12-10
10 <150> PRIOR APPLICATION NUMBER: US/09/162,021B
11 <151> PRIOR FILING DATE: 1998-09-28
12 <150> PRIOR APPLICATION NUMBER: PCT/US97/05031
13 <151> PRIOR FILING DATE: 1997-03-27
14 <150> PRIOR APPLICATION NUMBER: 08/622,738
15 <151> PRIOR FILING DATE: 1996-03-27
16 <160> NUMBER OF SEQ ID NOS: 19
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 4134
21 <212> TYPE: DNA
22 <213> ORGANISM: squalas acanthias
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (439)...(3522)
26 <400> SEQUENCE: 1
27      aattccgttg ctgtcgggttc agtccaagtc tcctccagtg caaaatgaga aatgggtggtc 60
28      gccattacag gaacatgcac tacatctgtg ttaatgaaat attgtcagtt atctgaaggt 120
29      tattaaaatg tttctgcaag gatggcttca cgagaaatca attctgcacg ttttccatt 180
30      gtcattgtat gaataactga ccaaagggat gtaacaaaat ggaacaaagc tgaggaccac 240
31      gttcaccctt tcttgagca tacgatcaac cctgaaggag atggaagact tgaggaggaa 300
32      atggggattg atcttccagg agttctgctg taaagcgatc cctcaccatt acaaagataa 360
33      gcagaaatcc tccaggcatc ctctgtaaac gggctggcgt agtgtggctt ggtcaaggaa 420
34      cagagacagg gctgcaca atg gct cag ctt cac tgc caa ctc tta ttc ttg 471
35      Met Ala Gln Leu His Cys Gln Leu Leu Phe Leu
36      1 5 10
37      gga ttt aca ctc cta cag tcg tac aat gtc tca ggg tat ggt cca aac 519
38      Gly Phe Thr Leu Leu Gln Ser Tyr Asn Val Ser Gly Tyr Gly Pro Asn
39      15 20 25
40      caa agg gcc cag aag aaa gga gac atc ata ctg gga ggt ctc ttc cca 567
41      Gln Arg Ala Gln Lys Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro
42      30 35 40
43      ata cac ttt gga gta gcc gcc aag gat cag gac tta aaa tcg aga ccg 615
44      Ile His Phe Gly Val Ala Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro
45      45 50 55

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46	gag gcg aca aaa tgt att cgg tac aat ttt cga ggc ttc cga tgg ctc	663
47	Glu Ala Thr Lys Cys Ile Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu	
48	60 65 70 75	
49	cag gcg atg ata ttc gca att gaa gag att aac aac agt atg act ttc	711
50	Gln Ala Met Ile Phe Ala Ile Glu Glu Ile Asn Asn Ser Met Thr Phe	
51	80 85 90	
52	ctg ccc aat atc acc ctg gga tat cgc ata ttt gac acg tgt aac acc	759
53	Leu Pro Asn Ile Thr Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr	
54	95 100 105	
55	gtg tcc aag gcg cta gag gca aca ctc agc ttt gtg gcc cag aac aaa	807
56	Val Ser Lys Ala Leu Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys	
57	110 115 120	
58	atc gac tcg ctg aac tta gat gag ttc tgt aac tgc tct gac cat atc	855
59	Ile Asp Ser Leu Asn Leu Asp Glu Phe Cys Asn Cys Ser Asp His Ile	
60	125 130 135	
61	cca tcc aca ata gca gtg gtc ggg gca acc ggg tca gga atc tcc acg	903
62	Pro Ser Thr Ile Ala Val Val Gly Ala Thr Gly Ser Gly Ile Ser Thr	
63	140 145 150 155	
64	gct gtg gcc aat cta ttg gga tta ttt tac att cca cag gtc agc tat	951
65	Ala Val Ala Asn Leu Leu Gly Leu Phe Tyr Ile Pro Gln Val Ser Tyr	
66	160 165 170	
67	gcc tcc tcg agc agg ctg ctc agc aac aag aat gag tac aag gcc ttc	999
68	Ala Ser Ser Ser Arg Leu Leu Ser Asn Lys Asn Glu Tyr Lys Ala Phe	
69	175 180 185	
70	ctg agg acc atc ccc aat gat gag caa cag gcc acg gcc atg gcc gag	1047
71	Leu Arg Thr Ile Pro Asn Asp Glu Gln Gln Ala Thr Ala Met Ala Glu	
72	190 195 200	
73	atc atc gag cac ttc cag tgg aac tgg gtg gga acc ctg gca gcc gac	1095
74	Ile Ile Glu His Phe Gln Trp Asn Trp Val Gly Thr Leu Ala Ala Asp	
75	205 210 215	
76	gat gac tat ggc cgc cca ggc att gac aag ttc cgg gag gag gcc gtt	1143
77	Asp Asp Tyr Gly Arg Pro Gly Ile Asp Lys Phe Arg Glu Glu Ala Val	
78	220 225 230 235	
79	aag agg gac atc tgt att gac ttc agt gag atg atc tct cag tac tac	1191
80	Lys Arg Asp Ile Cys Ile Asp Phe Ser Glu Met Ile Ser Gln Tyr Tyr	
81	240 245 250	
82	acc cag aag cag ttg gag ttc atc gcc gac gtc atc cag aac tcc tcg	1239
83	Thr Gln Lys Gln Leu Glu Phe Ile Ala Asp Val Ile Gln Asn Ser Ser	
84	255 260 265	
85	gcc aag gtc atc gtg gtc ttc tcc aat ggc ccc gac ctg gag ccg ctc	1287
86	Ala Lys Val Ile Val Val Phe Ser Asn Gly Pro Asp Leu Glu Pro Leu	
87	270 275 280	
88	atc cag gag ata gtt cgg aga aac atc acc gat cgg atc tgg ctg gcc	1335
89	Ile Gln Glu Ile Val Arg Arg Asn Ile Thr Asp Arg Ile Trp Leu Ala	
90	285 290 295	
91	agc gag gct tgg gcc agc tct tcg ctc att gcc aag cca gag tac ttc	1383
92	Ser Glu Ala Trp Ala Ser Ser Ser Leu Ile Ala Lys Pro Glu Tyr Phe	
93	300 305 310 315	
94	cac gtg gtc ggc ggc acc atc ggc ttc gct ctc agg gcg ggg cgt atc	1431

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95      His Val Val Gly Gly Thr Ile Gly Phe Ala Leu Arg Ala Gly Arg Ile
96                      320                      325                      330
97      cca ggg ttc aac aag ttc ctg aag gag gtc cac ccc agc agg tcc tcg      1479
98      Pro Gly Phe Asn Lys Phe Leu Lys Glu Val His Pro Ser Arg Ser Ser
99                      335                      340                      345
100     gac aat ggg ttt gtc aag gag ttc tgg gag gag acc ttc aac tgc tac      1527
101     Asp Asn Gly Phe Val Lys Glu Phe Trp Glu Glu Thr Phe Asn Cys Tyr
102                      350                      355                      360
103     ttc acc gag aag acc ctg acg cag ctg aag aat tcc aag gtg ccc tcg      1575
104     Phe Thr Glu Lys Thr Leu Thr Gln Leu Lys Asn Ser Lys Val Pro Ser
105                      365                      370                      375
106     cac gga ccg gcg gct caa ggg gac ggc tcc aag gcg ggg aac tcc aga      1623
107     His Gly Pro Ala Ala Gln Gly Asp Gly Ser Lys Ala Gly Asn Ser Arg
108     380                      385                      390                      395
109     cgg aca gcc cta cgc cac ccc tgc act ggg gag gag aac atc acc agc      1671
110     Arg Thr Ala Leu Arg His Pro Cys Thr Gly Glu Glu Asn Ile Thr Ser
111                      400                      405                      410
112     gtg gag acc ccc tac ctg gat tat aca cac ctg agg atc tcc tac aat      1719
113     Val Glu Thr Pro Tyr Leu Asp Tyr Thr His Leu Arg Ile Ser Tyr Asn
114                      415                      420                      425
115     gta tac gtg gcc gtc tac tcc att gct cac gcc ctg caa gac atc cac      1767
116     Val Tyr Val Ala Val Tyr Ser Ile Ala His Ala Leu Gln Asp Ile His
117                      430                      435                      440
118     tct tgc aaa ccc ggc acg ggc atc ttt gca aac gga tct tgt gca gat      1815
119     Ser Cys Lys Pro Gly Thr Gly Ile Phe Ala Asn Gly Ser Cys Ala Asp
120     445                      450                      455
121     att aaa aaa gtt gag gcc tgg cag gtc ctc aac cat ctg ctg cat ctg      1863
122     Ile Lys Lys Val Glu Ala Trp Gln Val Leu Asn His Leu Leu His Leu
123     460                      465                      470                      475
124     aag ttt acc aac agc atg ggt gag cag gtt gac ttt gac gat caa ggt      1911
125     Lys Phe Thr Asn Ser Met Gly Glu Gln Val Asp Phe Asp Asp Gln Gly
126     480                      485                      490
127     gac ctc aag ggg aac tac acc att atc aac tgg cag ctc tcc gca gag      1959
128     Asp Leu Lys Gly Asn Tyr Thr Ile Ile Asn Trp Gln Leu Ser Ala Glu
129     495                      500                      505
130     gat gaa tcg gtg ttg ttc cat gag gtg ggc aac tac aac gcc tac gct      2007
131     Asp Glu Ser Val Leu Phe His Glu Val Gly Asn Tyr Asn Ala Tyr Ala
132     510                      515                      520
133     aag ccc agt gac cga ctc aac atc aac gaa aag aaa atc ctc tgg agt      2055
134     Lys Pro Ser Asp Arg Leu Asn Ile Asn Glu Lys Lys Ile Leu Trp Ser
135     525                      530                      535
136     ggc ttc tcc aaa gtg gtt cct ttc tcc aac tgc agt cga gac tgt gtg      2103
137     Gly Phe Ser Lys Val Val Pro Phe Ser Asn Cys Ser Arg Asp Cys Val
138     540                      545                      550                      555
139     ccg ggc acc agg aag ggg atc atc gag ggg gag ccc acc tgc tgc ttt      2151
140     Pro Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr Cys Cys Phe
141     560                      565                      570
142     gaa tgc atg gca tgt gca gag gga gag ttc agt gat gaa aac gat gca      2199
143     Glu Cys Met Ala Cys Ala Glu Gly Glu Phe Ser Asp Glu Asn Asp Ala

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144		575		580		585		
145	agt	gcg	tgt	aca	aag	tgc	ccg	aat gat ttc tgg tcg aat gag aac cac 2247
146	Ser	Ala	Cys	Thr	Lys	Cys	Pro	Asn Asp Phe Trp Ser Asn Glu Asn His
147		590		595		600		
148	acg	tcg	tgc	atc	gcc	aag	gag	tac ctg tcg tgg acg gag ccc 2295
149	Thr	Ser	Cys	Ile	Ala	Lys	Glu	Ile Glu Tyr Leu Ser Trp Thr Glu Pro
150		605		610		615		
151	ttc	ggg	atc	gct	ctg	acc	atc	ttc gcc gta ctg ggc atc ctg atc acc 2343
152	Phe	Gly	Ile	Ala	Leu	Thr	Ile	Phe Ala Val Leu Gly Ile Leu Ile Thr
153		620		625		630		635
154	tcc	ttc	gtg	ctg	ggg	gtc	ttc	atc aag ttc agg aac act ccc atc gtg 2391
155	Ser	Phe	Val	Leu	Gly	Val	Phe	Ile Lys Phe Arg Asn Thr Pro Ile Val
156			640			645		650
157	aag	gcc	acc	aac	cgg	gag	ttg	tcc tac ctg ctg ctc ttc tcc ctc atc 2439
158	Lys	Ala	Thr	Asn	Arg	Glu	Leu	Ser Tyr Leu Leu Leu Phe Ser Leu Ile
159			655			660		665
160	tgc	tgc	ttc	tcc	agc	tcg	ctc	atc ttc atc ggc gag ccc agg gac tgg 2487
161	Cys	Cys	Phe	Ser	Ser	Ser	Leu	Ile Phe Ile Gly Glu Pro Arg Asp Trp
162			670			675		680
163	acc	tgt	cgg	ctc	cgc	caa	ccg	gcc ttt ggc atc agc ttc gtc ctg tgc 2535
164	Thr	Cys	Arg	Leu	Arg	Gln	Pro	Ala Phe Gly Ile Ser Phe Val Leu Cys
165			685			690		695
166	atc	tcc	tgc	atc	ctg	gtg	aag	acc aac cgg gtg ctg ctg gtc ttc gag 2583
167	Ile	Ser	Cys	Ile	Leu	Val	Lys	Thr Asn Arg Val Leu Leu Val Phe Glu
168			700			705		710 715
169	gcc	aag	atc	ccc	acc	agc	ctc	cac cgc aag tgg gtg ggc ctc aac ctg 2631
170	Ala	Lys	Ile	Pro	Thr	Ser	Leu	His Arg Lys Trp Val Gly Leu Asn Leu
171			720			725		730
172	cag	ttc	ctc	ctg	gtc	ttc	ctc	tgc atc ctg gtg caa atc gtc acc tgc 2679
173	Gln	Phe	Leu	Leu	Val	Phe	Leu	Cys Ile Leu Val Gln Ile Val Thr Cys
174			735			740		745
175	atc	atc	tgg	ctc	tac	acc	gcg	cct ccc tcc agc tac agg aac cat gag 2727
176	Ile	Ile	Trp	Leu	Tyr	Thr	Ala	Pro Pro Ser Ser Tyr Arg Asn His Glu
177			750			755		760
178	ctg	gag	gac	gag	gtc	atc	ttc	atc acc tgc gac gag ggc tcg ctc atg 2775
179	Leu	Glu	Asp	Glu	Val	Ile	Phe	Ile Thr Cys Asp Glu Gly Ser Leu Met
180			765			770		775
181	gcg	ctg	ggc	ttc	ctc	atc	ggc	tac acc tgc ctc ctc gcc gcc atc tgc 2823
182	Ala	Leu	Gly	Phe	Leu	Ile	Gly	Tyr Thr Cys Leu Leu Ala Ala Ile Cys
183			780			785		790 795
184	ttc	ttc	ttc	gcc	ttc	aag	tcc	cgt aag ctg ccg gag aac ttc aac gag 2871
185	Phe	Phe	Phe	Ala	Phe	Lys	Ser	Arg Lys Leu Pro Glu Asn Phe Asn Glu
186				800				805 810
187	gct	aag	ttc	atc	acc	ttc	agc	atg ttg atc ttc ttc atc gtc tgg atc 2919
188	Ala	Lys	Phe	Ile	Thr	Phe	Ser	Met Leu Ile Phe Phe Ile Val Trp Ile
189			815					820 825
190	tcc	ttc	atc	ccc	gcc	tat	gtc	agc acc tac ggc aag ttt gtg tcg gcc 2967
191	Ser	Phe	Ile	Pro	Ala	Tyr	Val	Ser Thr Tyr Gly Lys Phe Val Ser Ala
192			830					835 840

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193      gtg gag gtg att gcc atc ctg gcc tcc agc ttc ggg ctg ctg ggc tgc      3015
194      Val Glu Val Ile Ala Ile Leu Ala Ser Ser Phe Gly Leu Leu Gly Cys
195      845                                850                                855
196      att tac ttc aac aag tgt tac atc atc ctg ttc aag ccg tgc cgt aac      3063
197      Ile Tyr Phe Asn Lys Cys Tyr Ile Ile Leu Phe Lys Pro Cys Arg Asn
198      860                                865                                870                                875
199      acc atc gag gag gtg cgc tgc agc acg gcg gcc cac gcc ttc aag gtg      3111
200      Thr Ile Glu Glu Val Arg Cys Ser Thr Ala Ala His Ala Phe Lys Val
201      880                                885                                890
202      gcg gcc cgg gcc acc ctc cgg cgc agc gcc gcg tct cgc aag cgc tcc      3159
203      Ala Ala Arg Ala Thr Leu Arg Arg Ser Ala Ala Ser Arg Lys Arg Ser
204      895                                900                                905
205      agc agc ctg tgc ggc tcc acc atc tcc tcg ccc gcc tcg tcc acc tgc      3207
206      Ser Ser Leu Cys Gly Ser Thr Ile Ser Ser Pro Ala Ser Ser Thr Cys
207      910                                915                                920
208      ggg ccg ggc ctc acc atg gag atg cag cgc tgc agc acg cag aag gtc      3255
209      Gly Pro Gly Leu Thr Met Glu Met Gln Arg Cys Ser Thr Gln Lys Val
210      925                                930                                935
211      agc ttc ggc agc ggc acc gtc acc ctg tcg ctc agc ttc gag gag aca      3303
212      Ser Phe Gly Ser Gly Thr Val Thr Leu Ser Leu Ser Phe Glu Glu Thr
213      940                                945                                950                                955
214      ggc cga tac gcc acc ctc agc cgc acg gcc cgc agc agg aac tcg gcg      3351
215      Gly Arg Tyr Ala Thr Leu Ser Arg Thr Ala Arg Ser Arg Asn Ser Ala
216      960                                965                                970
217      gat ggc cgc agc ggc gac gac ctg cca tct aga cac cac gac cag ggc      3399
218      Asp Gly Arg Ser Gly Asp Asp Leu Pro Ser Arg His His Asp Gln Gly
219      975                                980                                985
220      ccg cct cag aaa tgc gag ccc cag ccc gcc aac gat gcc cga tac aag      3447
221      Pro Pro Gln Lys Cys Glu Pro Gln Pro Ala Asn Asp Ala Arg Tyr Lys
222      990                                995                                1000
223      gcg gcg ccg acc aag ggc acc cta gag tcg ccg ggc ggc agc aag gag      3495
224      Ala Ala Pro Thr Lys Gly Thr Leu Glu Ser Pro Gly Gly Ser Lys Glu
225      1005                                1010                                1015
226      cgc ccc aca act atg gag gaa acc taa tccaactcct ccatcaaccc      3542
227      Arg Pro Thr Thr Met Glu Glu Thr *
228      1020                                1025
229      caagaacatc ctccacggca gcaccgtcga caactgacat caactcctaa cgggtggctg      3602
230      cccaacctct cccctctccg gcactttgcg ttttgctgaa gattgcagca tctgcagttc      3662
231      cttttatccc tgattttctg acttgatat ttactagtgt gcgatggaat atcacaacat      3722
232      aatgagttgc acaattaggt gagcagagtt gtgtcaaagt atctgaacta tctgaagtat      3782
233      ctgaactact ttattctctc gaattgtatt acaaacattt gaagtatttt tagtgacatt      3842
234      atgttctaac attgtcaaga taatttgta caacatataa ggtaccacct gaagcagtga      3902
235      ctgagattgc cactgtgatg acagaactgt tttataacat ttatcattga aacctggatt      3962
236      gcaacaggaa tataatgact gtaacaaaaa aattgttgat tatcttaaaa atgcaaattg      4022
237      taatcagatg tgtaaaattg gtaattactt ctgtacatta aatgcatatt tcttgataaa      4082
238      aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaagcggcc cgacagcaac gg      4134
240 <210> SEQ ID NO: 2
241 <211> LENGTH: 1027
242 <212> TYPE: PRT

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/016,496

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 62
Seq#:7; Xaa Pos. 11,86
Seq#:8; Xaa Pos. 86
Seq#:11; Xaa Pos. 422,433
Seq#:12; Xaa Pos. 422,433
Seq#:15; N Pos. 3
Seq#:16; N Pos. 4,10

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/016,496

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Input Set : N:\Crf3\RULE60\10016496.raw

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L:394 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:192
L:565 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:49
L:580 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:289
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:80
L:793 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1297
L:796 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:1308
L:860 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:416
L:862 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:432
L:899 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:902 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:905 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:908 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:922 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:925 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:928 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:931 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:934 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:16
L:935 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:948 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:951 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:17
L:965 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
L:968 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
L:971 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
L:974 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
L:977 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:18
L:991 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:994 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:997 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:1000 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:1003 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19